

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/875,849ADATE: 01/15/99
TIME: 14:53:50

INPUT SET: S30805.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Briskin, Michael J.
Ringler, Douglas J.
Picarella, Dominic
Newman, Walter

(ii) TITLE OF INVENTION: Mucosal Vascular Addressins and Uses
Thereof

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
(B) STREET: Two Militia Drive
(C) CITY: Lexington
(D) STATE: Massachusetts
(E) COUNTRY: U.S.A.
(F) ZIP: 02421-4799

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/875,849
(B) FILING DATE: 12-FEB-1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/523,004
(B) FILING DATE: 01-SEP-1995

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/386,857
(B) FILING DATE: 10-FEB-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brook, David E.
(B) REGISTRATION NUMBER: 22,592
(C) REFERENCE/DOCKET NUMBER: LKS94-04A2

RAW SEQUENCE LISTING PATENT APPLICATION *US/08/875,849A*

 DATE: 01/15/99
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47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: 781-861-6240

49 (B) TELEFAX: 781-861-9540

50

51

52 (2) INFORMATION FOR SEQ ID NO:1:

53

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 1624 base pairs

56 (B) TYPE: nucleic acid

57 (C) STRANDEDNESS: double

58 (D) TOPOLOGY: linear

59

60 (ii) MOLECULE TYPE: cDNA

61

62

63 (ix) FEATURE:

64 (A) NAME/KEY: CDS

65 (B) LOCATION: 1..1218

66

67

68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

69

70 ATG GAT TTC GGA CTG GCC CTC CTG CTG GCG GGG CTT CTG GGG CTC CTC 48

71 Met Asp Phe Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu

72 1 5 10 15

73

74 CTC GGC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG GAG CCC CCG GAG 96

75 Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu

76 20 25 30

77

78 CCG GTG GTG GCC GTG GCC TTG GGC GCC TCG CGC CAG CTC ACC TGC CGC 144

79 Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg

80 35 40 45

81

82 CTG GCC TGC GCG GAC CGC GGG GCC TCG GTG CAG TGG CGG GGC CTG GAC 192

83 Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp

84 50 55 60

85

86 ACC AGC CTG GGC GCG GTG CAG TCG GAC ACG GGC CGC AGC GTC CTC ACC 240

87 Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr

88 65 70 75 80

89

90 GTG CGC AAC GCC TCG CTG TCG GCG GCC GGG ACC CGC GTG TGC GTG GGC 288

91 Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly

92 85 90 95

93

94 TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CAG CTC CTT GTG TAC 336

95 Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr

96 100 105 110

97

98 GCC TTC CCG GAC CAG CTG ACC GTC TCC CCA GCA GCC CTG GTG CCT GGT 384

99 Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly

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100	115	120	125	
101				
102	GAC CCG GAG GTG GCC TGT ACG GCC CAC AAA GTC ACG CCC GTG GAC CCC			432
103	Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro			
104	130	135	140	
105				
106	AAC GCG CTC TCC TTC TCC CTG CTC GTC GGG GGC CAG GAA CTG GAG GGG			480
107	Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly			
108	145	150	155	160
109				
110	GCG CAA GCC CTG GGC CCG GAG GTG CAG GAG GAG GAG GAG GAG CCC CAG			528
111	Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Glu Pro Gln			
112	165	170	175	
113				
114	GGG GAC GAG GAC GTG CTG TTC AGG GTG ACA GAG CGC TGG CGG CTG CCG			576
115	Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro			
116	180	185	190	
117				
118	CCC CTG GGG ACC CCT GTC CCG CCC GCC CTC TAC TGC CAG GCC ACG ATG			624
119	Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met			
120	195	200	205	
121				
122	AGG CTG CCT GGC TTG GAG CTC AGC CAC CGC CAG GCC ATC CCC GTC CTG			672
123	Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu			
124	210	215	220	
125				
126	CAC AGC CCG ACC TCC CCG GAG CCT CCC GAC ACC ACC TCC CCG GAG CCT			720
127	His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro			
128	225	230	235	240
129				
130	CCC AAC ACC ACC TCC CCG GAG TCT CCC GAC ACC ACC TCC CCG GAG TCT			768
131	Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser			
132	245	250	255	
133				
134	CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CAG GAG CCT			816
135	Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro			
136	260	265	270	
137				
138	CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CCG GAG CCT			864
139	Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro			
140	275	280	285	
141				
142	CCC GAC AAG ACC TCC CCG GAG CCC GCC CCC CAG CAG GGC TCC ACA CAC			912
143	Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His			
144	290	295	300	
145				
146	ACC CCC AGG AGC CCA GGC TCC ACC AGG ACT CGC CGC CCT GAG ATC TCC			960
147	Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser			
148	305	310	315	320
149				
150	CAG GCT GGG CCC ACG CAG GGA GAA GTG ATC CCA ACA GGC TCG TCC AAA			1008
151	Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys			
152	325	330	335	

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153
154 CCT GCG GGT GAC CAG CTG CCC GCG GCT CTG TGG ACC AGC AGT GCG GTG      1056
155 Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val
156           340           345           350
157
158 CTG GGA CTG CTG CTC CTG GCC TTG CCC ACG TAT CAC CTC TGG AAA CGC      1104
159 Leu Gly Leu Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg
160           355           360           365
161
162 TGC CGG CAC CTG GCT GAG GAC GAC ACC CAC CCA CCA GCT TCT CTG AGG      1152
163 Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg
164           370           375           380
165
166 CTT CTG CCC CAG GTG TCG GCC TGG GCT GGG TTA AGG GGG ACC GGC CAG      1200
167 Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln
168           385           390           395           400
169
170 GTC GGG ATC AGC CCC TCC TGAGTGGCCA GCCTTTCCCC CTGTGAAAGC      1248
171 Val Gly Ile Ser Pro Ser
172           405
173
174 AAAATAGCTT GGACCCCTTC AAGTTGAGAA CTGGTCAGGG CAAACCTGCC TCCCATTCTA      1308
175
176 CTCAAAGTCA TCCCTCTGCT CACAGAGATG GATGCATGTT CTGATTGCCT CTTTGGAGAA      1368
177
178 GCTCATCAGA AACTCAAAAG AAGGCCACTG TTTGTCTCAC CTACCCATGA CCTGAAGCCC      1428
179
180 CTCCCTGAGT GGTCCCCACC TTTCTGGACG GAACCACGTA CTTTTTACAT ACATTGATTC      1488
181
182 ATGTCTCAGG TCTCCCTAAA AATGCGTAAG ACCAAGCTGT GCCCTGACCA CCCTGGGCCC      1548
183
184 CTGTCGTCAG GACCTCCTGA GGCTTTGGCA AATAAACCTC CTAAAATGAT AAAAAAAAAA      1608
185
186 AAAAAAAAAA AAAAAA      1624
187
188
189 (2) INFORMATION FOR SEQ ID NO:2:
190
191     (i) SEQUENCE CHARACTERISTICS:
192         (A) LENGTH: 406 amino acids
193         (B) TYPE: amino acid
194         (D) TOPOLOGY: linear
195
196     (ii) MOLECULE TYPE: protein
197
198     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
199
200 Met Asp Phe Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu
201   1           5           10           15
202
203 Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu
204           20           25           30
205

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206 Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg
207           35           40           45
208
209 Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp
210       50           55           60
211
212 Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr
213   65           70           75           80
214
215 Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly
216           85           90           95
217
218 Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr
219           100           105           110
220
221 Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly
222           115           120           125
223
224 Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro
225       130           135           140
226
227 Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly
228   145           150           155           160
229
230 Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Glu Pro Gln
231           165           170           175
232
233 Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro
234           180           185           190
235
236 Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met
237       195           200           205
238
239 Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu
240       210           215           220
241
242 His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro
243       225           230           235           240
244
245 Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser
246           245           250           255
247
248 Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro
249           260           265           270
250
251 Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro
252           275           280           285
253
254 Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His
255       290           295           300
256
257 Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser
258   305           310           315           320

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SEQUENCE VERIFICATION REPORT
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Original Text